

EXHIBIT 9

-145 ATGTC
 -140 CATGAACCTGC TGAGTGGATA AACAGCACCGG GATATCTCTG TCTAAAGAA TATTACTACA CCAGGAAAAG
 -70 GACACATTG ACAACAGAA AGGACCTGT CACAGAAAC CACAGTGTCC TGTGATGTG ACATTCGCC
 1 ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG GGC TGT GAC AAG 60
 1 Met Gly Asn Asn Cys Tyr Asn Val Val Ile Val Leu Leu Val Gly Cys Glu Lys 20

61 GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC GTC GAG CCT GGT ACT TGC AGA AAA AAC 120
 21 Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Cys Pro Gly Thr Phe Cys Arg Lys Tyr 40

121 AAT CCA GTC TGC AAG AGC TGC CCT CCA ATT ACC TIC TCC ACC ATA GGT GGA CAG CCG AAC 180
 41 Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Ser Ser Ile Gly Gly Gln Pro Asn 60

181 TGT AAC ATC TCC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT AGG 240
 61 Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Phe Cys Ser Ser Thr 80

241 CAC AAC GCG GAG TGT GAG TCC ATT GAA GCA TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA 300
 81 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg 100

301 TGT GAA AAG GAC TGC AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT ACC 360
 101 Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser 120

361 TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC TGG AGG AAC TGC TCT 420
 121 Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser 140

421 CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC 480
 141 Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro 160

481 CCT GTG CTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GCA 540
 161 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Pro Gly 180

541 GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GGG CTC TCG GCT TTG CTG CTG GCC 600
 181 Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser Ala Leu Leu Ala 200

601 CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC 660
 201 Leu Ile Phe Ile Thr Leu Leu Phe Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His 220

661 ATA TTC AAG CAA CCA TTT AAG AAG ACC ACT CGA GCA GCT CAA GAG GAA GAT GCT TGT AGC 720
 221 Ile Phe Lys Gln Pro Phe Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser 240

721 TGC CGA CCA CAG GAA GAA GGA GGA CGA GCA GGC TAT GAG CTG TGA TGTACTATC 780
 241 Cys Arg Cys Pro Gln Glu Glu Gly Gly Gly Gly Tyr Glu Leu ---

781 CTAGGAGATG TGTGGCCGA AACCGAGAAG CACTAGGACC CCACCATCCT GTGGAACAGC ACAAGCAACC 850
 851 CCACCAACCT GTTCTTACAC ATCATCCTAG ATGATGTGT GGCAGCGACC TCATCCAAGT CTCTTCTAAC 920
 921 GCTAACATAT TTGCTTTAC CTTTTTTAAA TCTTTTTTA AATTTAAATT TTATGTGTG GAGTGTGTTTG 990
 991 CCTGCTGTG TGCACACGTG TGTGTGTG TGTGTGTGAC ACTCTGTG CCTGAGGAGG TCAGAAGAGA 1060
 1061 AAGGGTTGGT TCCATAAGAA CTGGAGTTAT GGATGGCTGT GAGCCGnnn GATAGTCGG GACGGAGACC 1130
 1131 TGTCTTCTTA TTTAACGTG ACTGTATAT AAAAAGAAA TGATATTCTG GGAATTCTAG AGATTGTCT 1200
 1201 GACACCCCTC TAGTTAATGA TCTAACAGGA ATTGTGATA CGTAGTATAC TGATATGTG TATGTATATG 1270
 1271 TATATGTATA TATAAGACTC TTTTACTCTC AAAGTCACCC TAGACTGTCT GTGATTCTAGG TCAATTCTAT 1340
 1341 TGGACATTTT ACGTCACACA CACACACACA CACACACACA CACCTTTATA CTACGTACTGT TATCGGTAT 1410
 1411 TCTACGTCTA ATAATGGGT AGGGTAAAG GAAACCAAAG AGTCAGTGT ATTATGTGGA GGTGACAGA 1480
 1481 CTACCCCTC TGGGTACGTG GGGACAGACC TCCCTGGAC TGTCTAAAC TCCCTTCTAGA AGTCTCGTCA 1550
 1551 AGTTCCCCGA CGAACAGGAC AGAGGAGACA CAGTCCGAAA AGTTATTTT CCGGCAATC CTTCCTCTGT 1620
 1621 TTCGTCACAC TCCACCCCTC CTGGACACTT GAGTGTCTAC CTTGGCCCGG AAGGTCAAGGT CGTACCCGTC 1690
 1691 TGTAGGGCG GGGAGACAGA GCGCGGGGG AGCTACGAGA ATCCGACTCAC AGGGCGCCCG GGGCTTCGCA 1760
 1761 AATGAAACTT TTTAATCTC ACAAGTTCTG TCCGGCTCG GCGGAACCTAT GCGGTCGATC CTATTACCT 1830
 1831 TATCTGGCG CCAAGATAAA ACAACCAAAA GCCTGACTC CGGTACTAAT TCTCCCTGCC GCCCCCCCCTA 1900
 1901 AGCATACGCG GGGCATCTC ACTTTAACGAA CCTGGCCGGG TTCTGCTGG TCTCCCTTTC GAAACGGTT 1970
 1971 CTTACAAAAG TAATTAGTTC TTGCTTTACG CCTCCAAAGCT TCTGCTAGTC TATGGCAGCA TCAAGGCTGG 2040
 2041 TATTGCTAC GGCTGACCGC TACGCCGGCG CAATAAGGGT ACTGGCCGGC CGGTGCAAGG CCCTTGGT 2110
 2111 TCAGAAACCC AAGGCCCGG TCATACCAAC GTTCTGACTT TGATTCTGC CGGTACGTGG TGGTGGT 2180
 2181 CTAGCTCTT TCTCGATAGT TAG AC

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